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ANALYSIS OF BIOTELEMETRY DATA

WORKSHOP SUMMARY

OFFICE OF INFORMATION TRANSFER

U.S. FISH and WILDLIFE SERVICE

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ANALYSIS OF BIOTELEMETRY DATA

WORKSHOP SUMMARY

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Colorado Cooperative Fish and Wildlife Research Unit

and

Office of Information Transfer

for

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THE WORKSHOP AT A GLANCE: POINTS TO REMEMBER

1. Biotelemetry can be used to locate animals and observe movements; as such, data are three-dimensional, including x, y locations and time of observation.

2. Aerial tracking, on-the-ground hand-held, and triangulation provide 3 methods of estimating location. When practical, using more than 2 fixed towers is a preferred method, as precision of estimates is improved and reflected or bounce signals can be detected.

3. Information on simple movements, incorporating the time dimension, is easily obtained through telemetry. The technology is available to display and analyze these data using microcomputers.

4. Home range estimators require a large number of locations and are often biased because of biologically unrealistic assumptions. Moreover, the information obtained may be of dubious value, telling very little about what animals actually require from their habitat.

5. Telemetry can be useful in habitat analyses; providing unbiased estimates of habitat utilization provided a random sample is obtained. However, without experimental manipulation, only correlations can be inferred, not cause and effect.

6. Telemetry is useful in survival rate estimation, and software is available to permit hypothesis testing regarding differential survival.

7. Telemetry is also valuable for population estimation, using mark-recapture techniques. Computer software is available to simulate changes in populations over time.

8. There is no single computer package to meet all the needs of researchers using biotelemetry. Some useful programs are listed in Table 1.

9. From Discussion:

A. Experimental design: it is important to know what you want to find out before you begin. If you can't answer a question within a satisfactory confidence interval, perhaps you should reconsider doing the study.

B. Correlation (factor x is associated with factor y) is much easier to establish than a cause and effect relationship (x is caused by y). Cause and effect can only be inferred if experimental manipulation has taken place.

Table 1. Software packages of use in telemetry data analysis.

Program	Purpose
BIOPLOT	Interactive plot of data on screen for error checking
BIOCHECK	Error detection via distances moved and/or speed limit
FIELDS	Prepare data for BIOPLOT, BIOCHECK, and HOMER
HOMER	Home range estimation
McPAAL	Home range estimation
DC80	Home range estimation
SURVIVE	Survival rate estimation, comparing groups
MICROMORT	Survival rate estimation, comparing rates by cause of death
LOTUS 1-2-3	Plotting telemetry data
FREELANCE	Publication quality graphics of data

C. It is better to answer one small question than to have multiple hypotheses and no clear conclusions for any of them.

INTRODUCTION

Telemetry is a tool we can use to locate animals and observe their movement. Without manipulations and controls, data obtained are strictly correlational and will not provide cause-and-effect results. Although telemetry can add to our understanding of what animals do, without carefully designed experiments, it does not help us understand why they do things (Sanderson 1966). The importance of carefully

designed experiments to establish cause and effect relationships will be stressed throughout the workshop.

Telemetry data are three-dimensional: x and y are spatial dimensions and time (t) is the third dimension, often overlooked. This may pose problems in some analyses. Data points obtained close together in time may not be independent, i.e., they may not contribute as much information as two locations taken further apart in time.

An excellent system for recording telemetry locations is the Universal Transverse Mercator (UTM) coordinate system (Snyder 1982). UTM coordinates are given on U.S.G.S. topographic maps, and allow simple calculations to determine the distance between two locations. UTM coordinates consist of two 7-digit numbers (specific to a zone) with units of meters. More or less precise designations are made by adding or subtracting digits.

LOCATION ESTIMATION

There are three basic ways of estimating location: the least quantifiable is on-the-ground location simply saying, it's over there . However, this approach can also be the most accurate when the animal is actually seen.

The second method, triangulation, uses fixed or mobile towers to estimate location as the point of intersection of observed bearings. Accuracy is a function of the distance from the towers taking the bearings, the precision of the bearings, and the angle of their intersection.

A major problem with 2-tower triangulation is that reflected (bounce) signals cannot be detected and eliminated (Lee et al. 1985). Thus, some modern triangulation systems use n towers ($n > 2$) to increase accuracy. Error can be minimized with judicious tower placement. By developing contour maps, triangulation precision can be estimated in advance (White 1985). This advance preparation can help the investigator to determine whether the degree of precision that will be obtained is adequate, or whether in fact the project should be scrapped.

Lenth (1981) developed statistical estimators to help locate emergency locator beacons for downed aircraft (which frequently go down in bounce-prone areas). His robust estimators of location are useful in study sites with rugged terrain, obtaining fairly accurate estimates in the presence of some unreliable bearings.

The third location estimation technique is aerial tracking (Gilmer et al. 1981). Accuracy and precision of this method can only be determined with radios placed at known locations without the biologist knowing the true location. The Loranz navigation system solves the major problem of aerial tracking by providing the biologist with a readout of the UTM coordinates at the press of a button, thus pin-pointing his location on the map.

The software program BIOCHECK can be used to identify outliers caused by reflected signals or mis-recording the data. Using this program, the biologist can set limits such as a maximum speed limit or distance allowed between successive locations before the location is flagged as potentially being in error. If the animal appeared to move at an unlikely speed, or showed up in an unlikely place, the program will flag these to alert the investigator. A second software program, BIOPLOT, can be used to plot locations, with options to mark or delete suspect locations from the data file. Both programs run on IBM PC-compatible microcomputers.

SIMPLE MOVEMENTS

Biotelemetry is commonly used to answer such questions as rate of travel, proportion of time spent at a single location, and the proportion of time spent traveling. Unfortunately, the time dimension of the data is frequently lost in graphical presentation.

Microcomputers can be used to address this problem. The time dimension as well as animal interactions can be shown with plotted graphics. One type of still graphics uses vector plots. There are various ways of showing the time dimension; one approach is to connect consecutive locations with distinguishing lines. For example, elk movements with less than 10 days between locations could be shown with solid lines, 10-30 days with dashed lines, and more than 30 days with dotted lines. In dot plots on film, the intensity of color on the film determines the amount of activity, e.g., habitat utilization. These plots may not be of publishable quality, but they are useful for the

researcher to view his own data.

The Polaroid Palette provides a relatively inexpensive ($1300) film recorder for use with IBM PC-compatible microcomputers. The Palette can be used with a number of different graphics packages to produce presentation quality slides. Lotus 1-2-3 combined with FREELANCE is an effective method to produce slides of telemetry data, or publication quality figures with a pen plotter.

A relatively inexpensive new technique allows the third dimension (time) to emerge with animation using microcomputers. Data are easily comprehended, and interactions between animals can be evaluated. However, artifacts of data collection may emerge. If collections were made too far apart in time, animation will give the impression of very rapid movement.

The use of animation (movies) is the most effective way of showing the time dimension. Many slides are generated, then flipped through rapidly to give the appearance of animation (White 1979). This is useful for assessing large migration patterns, or, on a smaller scale, for habitat utilization studies. Time-specific interaction between animals is stressed. Movies are a very effective I&E tool. The primary drawback is cost. Video-taping is emerging as a cost-effective alternative.

HOME RANGE ESTIMATION

Existing home range estimators, using biotelemetry data, are not very precise, as the following discussion will demonstrate. The investigator may wish to reassess and consider the purpose of making the estimate. Home range really does not tell us much about what animals do, or about what they require from an area.

1. Minimum area polygon (Mohr 1947)

Description: This method delineates a convex shape by connecting all points on the outside edge. The area within the polygon is then calculated.

Problems: 1) As additional points are obtained, the area automatically increases (Jennrich and Turner 1969). Thus, the larger the sample size, the larger the expected home range that is identified.

2) Data points may not be statistically independent. Points collected close together in time do not represent independent observations, and thus the sample size is artifically inflated.

3) Related to this is the problem of outliers, which distort the configuration. But how can one determine which points are to be deleted from the home range? One option is to design a 95% polygon, and throw out 5% of the points. But biologically, there is no reasonable method to decide which points to eliminate. Moreover, the time it takes a computer to generate all possible maps using all possible combinations of 95% of the points is prohibitive.

4) The convex polygon may encompass area which is not actual habitat, such as water. The biologist can look at the map that was generated, eliminate certain points, and redraw the map. The danger lies in making subjective judgments about which points are valid. One could almost draw the map on the basis of field man saavy, and skip the home range estimator.

5) Finally, there is no way of putting any kind of precision estimate on the resulting polygon. How useful is the estimate without a confidence interval and associated variance?

2. Ellipses

Description: Hayne (1949) first described circular home ranges for small mammals. Jennrich and Turner (1969) developed a noncircular plotting method in which home range area was not a function of sample size. Locations are assumed to be identically and independently distributed according to a bivariate normal probability distribution. Dunn and Gipson (1977) developed a method accommodating time series data. By modeling the time series nature of the data, the assumption of independent observations can be relaxed somewhat.

Problems: The major problem with the bivariate normal method is the assumption that animal movements are random, and that the most likely area for an animal to be is near the middle (the mean x and y location). It also assumes homogeneous habitat. All three assumptions are obviously false. Dunn and Brisbin (1982) calculated that 98 locations would be necessary to achieve a 20% confidence interval; to achieve 10% confidence requires 386 fixes.

3. Nonparametric

Description: Siniff and Tester (1965) developed the grid cell method to analyze movement data. The area over which an animal has moved is dissected by a grid into cells, or blocks. The number of animal locations are tabulated for each of these cells, and the sum of the area of cells containing locations is taken as the estimate of home range area. Grid cell counts make no assumptions about the shape of the polygon. Anderson (1982) used the Fourier series to smooth the location fixes to form a surface representing home range. A third nonparametric technique, devised by Dixon and Chapman (1980) is based on the harmonic mean of the area distribution. The activity area isopleth is then related directly to the frequency of occurrence of an individual in that area.

Problems: Nonparametric estimators that rely on grid cells share some similar problems, such as subjectivity. How does one determine grid cell size, and how does one determine the origin of the grid cell coordinate system? Different estimates will be obtained depending on the cell size chosen: there is no biological basis for this decision. Siniff's method includes a fill option to permit interpolation between cells, but again, subjective decisions are involved: just how much fill-ing should be permitted? What criteria are used, and what is the biological basis for those criteria? Other problems include large sample size requirements (since no assumptions are made about the shape of the home range), lack of statistical independence of consecutive locations, and lack of precision estimates (confidence intervals). The Fourier series estimator avoids the grid cell problem.

In summary, there is no single preferred estimator of home range. All have their faults. However, if a method must be used, there are some criteria by which the most appropriate method may be selected:

1) Time series randomization test: if each point is independent, the average distance between points should be the same regardless of the order in which they are entered (Schoener 1981). Swihart and Slade (1985) have extended this test by making additional assumptions about the underlying statistical distribution of the locations.

2) Shape criterion: apply a chi-square goodness of fit test to determine whether the home range shape is close to the expected shape (Samuel and Garton 1985).

3) Sample size: the large sample size required for nonparametric estimators may preclude their use in a particular study. Estimators requiring additional assumptions may be preferred.

Home range is a concept that is frequently abused. Some of the problems go back to its definition as the area used by the animal in its normal activities (Burt 1943:351). What is use ? What is normal ? Normal is frequently defined as 95% of the time, but with no biological justification.

Many of the applications which have used home range estimates can be performed without them. For example, to test for shifts in animal's area of utilization, the MRPP test of Mielke and Berry (1982) can be used instead of comparing 2 home range estimates. The method is programmed in Berry (1982). To demonstrate energetic requirements, length of distance moved would be preferable to home range size.

HABITAT ANALYSIS

The four components of habitat analysis are: availability, utilization, preference, and critical habitat. It is important to remember that these components are not equivalent.

1. *Availability*: This consists of the amount of area of each habitat type that is available for use by the population or individual. It can be measured from a habitat map such as a digital surface cover map accessible with a Geographic Information System (GIS). Unfortunately, our perceptions are not necessarily the same as the animal's; that is, what may appear available to us may not, for some reason, actually be available to the animal.

2. *Utilization*: Telemetry data provide us with the utilization information, providing estimates of the amount of time spent in each habitat type. It is important to apply utilization study results correctly. Simple observation of which areas a population uses does not prove it would not use some other area under certain conditions.

3. *Preference*: Does the population actually prefer a particular habitat type? The best way to approach this problem is with a chi-square test, comparing observed use with expected use, based on the proportion of each habitat type

that is available for use (Neu et al. 1974, Marcum and Loftsgaarden 1980). Johnson (1980) developed a ranking method to test for preference when availability is poorly known, such as how much of a lake could be considered available mallard habitat. He reasoned that, although we can't define availability, we can rank available habitats. For other types of preference, see Alldredge and Ratti (1986).

4. *Critical Habitat*: The only way to determine whether a population actually requires a given habitat type is through manipulation. Undisturbed access to different habitat types is permitted first, and observations of preference are made. Then the population is deprived of its preferred habitat type and observed to see whether the population declines.

This type of habitat manipulation and experimental deprivation may not ever be practical, but without it, inferences about what constitutes critical habitat cannot be made. No cause and effect relationship can be established without experimentation; a correlation between what is available and what is used is the strongest inference that should be made.

SURVIVAL RATE ESTIMATION

A fundamental aspect of wildlife management is population management, which includes survival rate estimation. Telemetry is an excellent tool to use in making these estimates, first applied by Trent and Rongstad (1974) to cottontail rabbits. A major assumption that must be made when equipping an animal with a radio is that survival is not affected by this action.

Survival results are binomially distributed (the animal is either alive or dead after a period of time), and therefore results can be analyzed with a chi-square table. Survival rates can be calculated as time-specific or age-specific. Age-specific analysis has emerged from human studies using life tables, where survival is to a large extent a function of age. However, in wildlife populations, environmental effects (such as a bad winter) may override effects of age; thus time-specific differences become more important. For this reason, life tables are of less value for wildlife studies.

Survival rates can also be tested with the multinomial distribution by establishing categories, e.g., alive/dead in year 1, year 2, etc. Then, age or time-specific differences can be tested. The computations can get complicated; Program SURVIV has been developed to handle them (White 1983).

This software program can handle multinomial categories, permitting tests of age/time-specific differences. Hypotheses are easily tested, such as the comparative survival rate of males and females, or hunted and non-hunted populations.

A potential problem with any telemetry study is radio failure. The two possibilities are that the radio failed because the animal has died, or that the radio failed but the animal is still alive. We may not know which is really true. If the animal died, that information is entered into the appropriate cell; however, if the radio has failed and the animal is still alive, data from that animal must be discarded. The biologist has to make the best decision possible based on past experience. If it appears that a bad set of radios was used, that is, the entire cohort died, that cohort can be dropped from the data set and the program run without it.

Another common problem is the intermittent cohort: animals that migrate out of the population for a period of time, then reappear, the radio still working. Is emigration equivalent to death for purposes of analysis? The answer depends on the situation. Normally, emigration is treated as death because emigration is assumed to be permanent dispersal. However, if the situation is common, then a re-evaluation of what the population is should be made.

SURVIV can accommodate missing data, from a single entry to an entire cohort, as previously mentioned. Another advantage to SURVIV is that time boundaries can be set any way the researcher desires: by year, by week, or even unequally. And, the first cohort can be started as any time. SURVIV is capable of handling very complicated cell expressions, which actually can work to the disadvantage of an inexperienced user.

Radio loss or failure is normally a minor problem in telemetry research. This is contrasted with bird banding data which can also be used for survival rate estimation, but in which failure to have the band reported is the rule. Brownie et al. (1985) devised programs specifically to deal with banding data. Here the

observed cells are not expected to add up to one since the recovery rate will always be less than one. The confidence interval for survival is inversely proportional to recovery rate.

An interesting problem in survival studies is competing risk analysis. There will always be a Number 1 killer, whether it be predation, hunting, or accidents. Telemetry is of value in determining cause of death, and hence in studying compensatory versus additive mortality. Only by introducing a perturbation into the system can we determine to what degree mortality is additive or compensatory.

A second program useful for estimating mortality from different causes of death is MICROMORT, developed by Heisey and Fuller (1985). The program is interactive and runs on an IBM PC or compatible.

Survival data from radioed animals provide the status of the animal (alive or dead), and this is the information utilized in Program SURVIV to estimate and test survival rates. Also available is the length of life, or time that the animal lived after the radio was attached. Survival data from radioed animals is thus identical to clinical studies with human subjects that report back to the physician periodically, or laboratory studies where the experimental animals can be monitored through time. Thus the numerous statistical techniques utilized by the medical field are applicable to the analysis of some biotelemetry survival studies. Good texts to use to become acquainted with these approaches are Lee (1980) and Kalbfleisch and Prentice (1980).

Before embarking on a survival rate estimation study, the necessary sample size should be determined. If it is not possible to equip as many animals as is necessary to achieve the desired confidence interval, money will be wasted. If 500 radios are needed and you can only afford 100, you may as well save your money, or at least wait until the study can be done properly.

A final problem that must be addressed is the sample itself, which, to allow inference to the entire population, must be random. If the sex or age ratio of animals of animals caught in a trap can be manipulated, a random sample was probably not obtained. It is quite likely that most capture methods result in unrepresentative samples.

Population modeling can be done using a standard accounting spreadsheet program such as Lotus 1-2-3. Each cell can be defined in terms of any other cell, and its value set as either variable or absolute. For example, columns could be used to define the year of the simulation, while rows represent ages within the population. By manipulating the fecundity and survival variables, the impact on the population in year x can be simulated almost instantly. There is tremendous flexibility in this kind of system, limited perhaps only by your imagination.

POPULATION ESTIMATION

Radioed animals can be used as part of a capture-recapture study to estimate population size. The major assumptions in a capture-recapture study are: a closed population (no migration, mortality or natality), a known number of marks, and a random sample. One advantage of radio telemetry is in bolstering these assumptions, as the marked animals can be verified to be in the population before a second sample is taken. Rice and Harder (1977) used multiple second samples in their recapture study and devised an average estimate of population level.

Another method of combining independent samples is to use rank order statistics and find the median of the estimates and its confidence interval (Conover 1971).

Some problems with capture-recapture techniques:

1) A fairly large proportion (>20%) of the population needs to be marked in order to achieve a high proportion of marks in the second sample.
2) Animals have different capture probabilities and sighting probabilities, which can bias the estimates (White et al. 1982). However, if the method of capturing the animals to place radios on them is statistically independent of the method of recapture (i.e., sighting them from the air), then the bias is not likely to be significant.
3) In some areas, there may be a problem with aesthetics. People don't like to see wild animals with collars around their necks.
4) There is a high cost associated with marking an adequate sample.

Just what is an adequate sample size? For populations of 100-500, approximately 20% of the population should be marked, and about 50% of the population should be observed to generate a 95% confidence interval that is within 20% of the estimate. Simulation of a proposed project can be performed with program CAPTURE (White et al. 1982) to show the results that could be expected before spending money on equipment.

Telemetry techniques can also be used to check assumptions of other population estimation techniques. For example, the two major assumptions of line transect estimation (Burnham et al. 1980) are: that animals on the line are always seen, and that animals do not move away from the line before being observed.

DISCUSSION

Q. You don't consider 1 ha as an acceptable error polygon for estimates of location from triangulation?
GW. The usefulness of a location estimate depends on what it will be used for. As an example, to study habitat utilization of cottontail rabbits, a 1 ha error polygon would be worthless. In contrast, a 1 ha error polygon for elk may be okay if the habitat is not too broken, i.e., habitat units are much larger than 1 ha.

Q. Why bother with a three tower system when the standard deviation of azimuths is small?
GW. The three tower system provides the capability to detect spurious bearings due to bounce and reflected signals. In addition, the size of the confidence ellipse will be about 1/3 of that from a two tower system.

Q. Doesn't the standard deviation of azimuths for a study area take into account bounce?
GW. The standard deviation of azimuths should only account for sampling error from the observer, i.e., error due to the listener's ability to pinpoint the direction of the signal. The error due to reflected signals is handled with the robust estimators of Lenth (1981). If the error from bounce signals is included in the standard deviation of the azimuths, then Lenth's robust estimators would generate biased estimates of location because large intersection areas would be attributed to the large standard deviation, not reflected signals.

Q. Why is it a problem that home range size keeps increasing (in the polygon method) with additional observations?
GW. The size of the home range is now a function of the number of locations taken, i.e., the parameter that is being estimated is a function of sample size. The actual parameter is changing as more data are collected. Thus, you are aiming at a moving target, and the faster you swing, the faster the target moves!

Q. How many locations do you need to estimate home range size adequately?
GW. What is an adequate home range estimate? If you define adequate as a 95% confidence interval of length 10% of the estimate, statistical techniques can be used to determine sample size (for the estimators that have an associated variance estimate). However, the question of adequacy is really a biological question, and must be answered on biological grounds. What will the estimate be used for, and how precise must the estimate be to meet these needs?

Q. What sample size do you need to calculate survival rates with SURVIV?
GW. Simple guidelines to calculate sample size for a survival rate from radioed animals can be based on the binomial distribution. The estimate of survival is

$$\hat{s} = \frac{n}{N}$$

where N is the number of radios, n is the number of animals that lived, and $\hat{s}$ is the estimate of survival. The variance of $\hat{s}$ is

$$var(\hat{s}) = \frac{\hat{s}(1 - \hat{s})}{N}$$

with a standard error of $se(\hat{s}) = \sqrt{var}(\hat{s})$. Then a 95% confidence interval can be constructed as $\hat{s}$ $1.96 \times se(\hat{s})$. Now suppose you desire to estimate s to $0.1s$. Setting the $1.96 \times se(\hat{s}) = 0.1s$ yields a solution for N (given an initial estimate of s):

$$N = \frac{1.96^2(1 - \hat{s})}{0.1^2\hat{s}}$$

As an example, if we expect $\hat{s}$ is about 0.4, then to get a 95% confidence interval of 10%, we need to put out N = 577 radios. After looking at that, we probably decide that a 10% interval is too good! Let's try for 20%. Then only 144 radios are needed to get a 95% interval of (0.32 - 0.48) instead of (0.36 - 0.44). Note that the size of the sample also depends on the value of

$\hat{s}$ because as the survival rate becomes smaller, the relative size of the confidence interval can be allowed to increase.

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BIOCHECK: Telemetry Data Checking

The BIOCHECK subprogram provides a method of checking the (x, y, t) vectors of biotelemetry data. Two basic methods of detecting errors in the data are provided. First, distances between locations are checked, with the rate of movement also considered. Second, the locations are checked to see if they are within a specified rectangle.

The input specifications to the BIOCHECK subprogram are

xcoor=x_UTM_field ycoor=y_UTM_field time=date_time_field
[age=age_field] [sex=sex_field] [id=animal_id_field]
[xmin=minimum_x] [xmax=maximum_x]
[ymin=minimum_y] [ymax=maximum_y]
[speedlim=speed_limit [mph|kmph|mps|m]]
[distance=maximum_distance_traveled [miles|km|m|feet]]
[maxanim=max_#_of_animals_or_subfiles]

The XCOOR, YCOOR, and TIME parameters specify the field numbers of the x and y coordinates, and the time field, respectively. XCOOR and YCOOR variables are assumed to be in units of meters. The TIME variable is assumed to have the format yymmdd.hhmm, where yy is the last 2 digits of the year, mm is the month (01-12), dd is the day (01-31), hh is the hour (00-23), and mm is the minute (00-59).

The AGE, SEX, and ID parameters specify the field numbers of the age, sex, and animal identification codes. These fields are checked to see that they do not change, hence, that a subfile contains only one animal. If the contents of these fields do change, then a message is printed and error checking continues. If one (or all) of these parameters is not specified, error checking is not provided for the missing field.

The XMIN, XMAX, YMIN, and YMAX parameters specify values for the rectangle to use in checking the geographic locations of fixes. That is, if an (x, y) pair is not inside of this rectangle, an error message is printed. Default values of these parameters are very large and small values, so that all locations are inside the rectangle. Multiple values of each of these parameters can be specified to handle multiple subfiles in one run. The first value is used for the first subfile, the second value is used for the second subfile, and so on. If enough values are not specified to provide for all subfiles, then the last value specified is used for all remaining subfiles.

The SPEEDLIM parameter specifies the fastest rate of movement at which an animal is assumed to move between fixes (locations). Rates of movement between 2 consecutive fixes (locations) greater than SPEEDLIM are flagged out as errors. After the numerical value, the units of the value can be specified to interpret the speedlimit parameter. As with the XMIN parameter, multiple values can be specified to provide each subfile to be processed with BIOCHECK a diffst allowable distance between 2 consecutive fixes (locations) before an error message is printed. The units specified with this parameter allow units other than the default of km. Also, multiple values are matched with their respective subfiles as for XMIN. A synonym for DISTANCE is MAXDIST.

The MAXANIM parameter specifies the maximum number of animals to be processed in one subfile of data. The default value is 100, that is, 100 different values of the ID variable can be handled within a single subfile. If more than 100 values of the ID variable occur within a subfile, then the larger value must be specified for the MAXANIM parameter. This parameter should seldom if ever be used.

Limitations of Program BIOCHECK

No methods are provided to test for locations inside an area that are not a feasible habitat. For example, the boundaries of a lake cannot be specified to check for locations occurring in the lake.

At this time, BIOCHECK only reads input data (i.e., locations) from the file named BIOCHECK.DAT. Hopefully an additional parameter to specify the input data file can be included eventually.

Output for Program BIOCHECK

Output of BIOCHECK consists of a summary for each animal checked of errors located in the data, plus a summary of the parametric values used in the check. This output is listed on the screen, although the > symbol can be used on the execution line to redirect the output to a file.

HOMER: Home Range Estimation

HOMER provides home range estimates from a set of (x, y, t) data. Available estimates are the minimum area polygon, Jennrich-Turner ellipse (Jennrich and Turner 1969), Dunn ellipse (Dunn and Gipson 1977), and a grid-cell estimator (Siniff and Tester 1965).

The general format of the HOMER calling sequence is

xcoor=x_UTM_field ycoor=y_UTM_field time=date_time_field
[age=age_field] [sex=sex_field] [id=animal_id_field]
[map=[fill|both]] [mapscale] [remove]
[xorigin=value(s)] [yorigin=value(s)]
[square=value(s) [mile|km|m|feet]] [grids=#_grid_cells]
[vectime=value(s) [day|days|hour|hours|minute|minutes]]
[vecdist=value(s) [mile|km|m|feet]] [fill=value(s)]
[dunntime=value [day|days|hour|hours|minute|minutes]]
[dunn] [residual] [likeliho] [diagnost]
[random] [lotus (jt jennrich polygon dunn unique data)]
[maxanim=max_#_animals] [maxcase=max_#_cases]

XCOOR, YCOOR, and TIME specify the variable names for x and y coordinates, and time, respectively. These parameters are the only ones that must be specified to obtain home range estimates. The default estimates are the minimum area polygon and the Jennrich-Turner estimate.

XCOOR and YCOOR are assumed to have units in meters and TIME in days. The TIME field must be in the format yymmdd.hhmm where yy is the last 2 digits of the year, mm is the month (01-12), dd is the day (01-31), hh is the hour (00-23), and mm is the minute (00-59).

Specification of any of the parameters from map= to fill= causes the estimation of home range with the grid cell method. The MAP parameter causes the grid cell home range map to be printed. MAP without an equal sign and second parameter prints the grid cell map without any f illed locations. MAP=FILL causes only the f illed map to be printed, and MAP=BOTH causes both maps to be printed. The MAPSCALE parameter causes the printed map to be scaled so that the x and y distances are approximately equal.

The XORIGIN and YORIGIN parameters provide the x and y coordinates for the lower left corner of the grid cell map. If they are not specified, the data file is read twice, once to obtain values for XORIGIN and YORIGIN, and once to generate the home range estimates. Note that both XORIGIN and YORIGIN parameters allow more than one value. Multiple values are used for successive subfiles, with remaining subfiles set to the last value in the list. Thus,

xorigin=700000 800000 9000000

sets the value of the left side of the grid cell map to 700000 for the first subfile, 800000 for the second subfile, and 900000 for the third and all remaining subfiles.

The REMOVE is the wild fix (location) removal option. Generally its use is not needed.

The SQUARE= parameter sets the size of the grid cell square used for home range estimation. The GRIDS= parameter sets the number of grids in one dimension to be used for home range estimation. The total number of grid cells is thus this value squared. Both SQUARE and GRIDS allow multiple values for multiple subfiles. The defaults for these parameters are GRIDS=100 and SQUARE equal to min $(y_{max} - y_{min}, x_{max} - x_{min})$/GRIDS.

The VECTIME parameter specifies the maximum amount of time allowed between fixes (locations) to perform vector fill. The default value is zero, in which, no vector fill is performed. A positive value for vector fill causes a fix (location) to be generated in a cell that is crossed by the line

connecting 2 consecutive locations within VECTIME time units. Although the TIME variable is assumed to have units of days, a value for VECTIME can be specified in hours or minutes by including the units after the value. Like the above parameters, VECTIME can have multiple values, one for each subfile.

The VECDIST parameter is another parameter allowing vector fill of grid cells where no locations were found. VECDIST sets the maximum distance of the vector along which vector fill can operate. The default value is zero, in which, no vector fill takes place.

The FILL parameter specifies the number of grid cells thinterpreted as the size of holes in the map that will be filled. Thus FILL=2 causes grid cells within 2 cells of filled cells to be filled, i.e., a fix (location) is generated for the empty cell. The default is zero, hence, no cells are filled. FILL also allows multiple values, one for each subfile.

The DUNNTIME parameter specifies the time interval between fixes (locations) within a burst for the Dunn home range estimator. Specification of this parameter causes the Dunn estimator to be calculated. The value specified is assumed to have units of days unless hours or minutes are added to the specification. The resulting value is used to divide the input data into bursts. Two consecutive locations within DUNNTIME units of each other are assumed to be in the same burst. Likewise two consecutive locations separated by more than DUNNTIME units are separated into different bursts.

A potential danger is that a constant time interval between locations within bursts will not be maintained. The Dunn method assumes all locations within a burst are a fixed time unit apart, and that the time between bursts is large enough to assume that data in separate bursts are independent. HOMER *does not* check these assumptions.

The lotus parameter generates data files that can be input to Lotus 1-2-3 for graphic presentation of the data or home range map. If the lotus parameter is specified without options (i.e., values within parentheses), then files are generated for each of the home range estimates. The various options within the parentheses are

Option	Meaning
jt	Jennrich-Turner ellipse
jennrich	Jennrich-Turner ellipse
unique	Jennrich-Turner ellipse for unique data only
polygon	Minimum area polygon
dunn	Dunn-Gipson ellipse
data	x-y coordinates of data file

These files can be read into Lotus 1-2-3 in the file import mode. The lotus workspace PLOT.WK1 included on the HOMER disk provides an example of how to handle these files for graphic output. If the Lotus 1-2-3 graphs are saved, they can be manipulated by FREELANCE to produce publication quality output.

Limitations for Subprogram HOMER

1) The harmonic mean estimator of Dixon and Chapman (1980) is not yet implemented.

2) The Fourier Series estimator of Anderson (1982) is not yet implemented.

3) The XORIGIN and YORIGIN values must be specified on the input, as the PC DOS version of HOMER does not yet do the 2 passes described above.

4) HOMER reads its input from the file named HOMER.DAT in the local directory. It should read input from a user-specified file, or the standard input.

Output from Subprogram HOMER

Output depends on the parameter specified. Generally the user will want to look at the output on the screen. However, by using the redirection capability of DOS (i.e., the > symbol) with the execution of HOMER (e.g., homer >temp.lis), the output can be saved in a file for later printing.

Program SURVIV User's Manual Version 1.2

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Program SURVIV (a stand alone program) is used to estimate survival rates from user specified cell probability functions. The program reads the user specified algebraic expressions and constructs a FORTRAN 77 subroutine that calculates the log-likelihood function. Numerical optimization is then used to estimate the unknown parameters. Currently the program is available for CDC-NOS, VAX-VMS, UNIX, PC-DOS, and MS-DOS operating systems. The NOS version is written in single precision, while the VMS, UNIX, and DOS versions are written in double precision.

The details of the syntax for each of the procedures in Program SURVIV are shown in Table 1. As the reader works through the examples illustrating these procedures, he should occasionally refer back to Table 1 to understand the information presented. Table 1 is a summary of each procedure and does not provide the detailed explanations provided in the examples.

Table 1. Summary of command syntax for each of the procedures and their modifiers in Program SURVIV. Modifiers enclosed in brackets indicate optional input. Program SURVIV allows comments enclosed between /* and */ symbols, and statements are delineated with semicolons.

```
PROC TITLE Any title information to be printed at top of each page;

PROC MODEL NPAR = # of S(I)'s in model;

        COHORT = # of animals in cohort;

                # observed: algebraic expression for cell probability;
                .
                .
                .
                repeated for up to maximum number of cells per cohort;

        COHORT = repeated for up to maximum number of cohorts;

        LABELS;
                S(1) = identifying label;
                .
                .
                .
                S(NPAR) = identifying label;

PROC ESTIMATE [NSIG = # of significant digits to find for estimates (default is 5)]
                [MAXFN = maximum number of function evaluations (default is 1000)]
                [NAME = name of submodel]
                [TRANSFORM = NONE or ABS (default is SIN transform)];
                [NOVAR (Do not print variance-covariance matrix, default is to print matrix)];

        INITIAL;
                S(1) = value;
                .
                .
                .
                S(NPAR) = value;

        or      ALL = value;

        or      RETAIN = modname /* Obtain initial estimates from output
                    of previous model named in "modname" */

        CONSTRAINTS /*Constraints of the form */;
                S(1) = S(2) /* S(1) is the same as S(2) */ ;
                S(1) < S(2) /* S(1) is less than S(2) */ ;
                S(1) > S(2) /* S(1) is greater than S(2) */;
                S(1) = value /* Fix parameter to constant */;
```

Table 1. Continued.

```
PROC TEST /* No modifiers */;

PROC BROWNIE [NSIG = # of significant digits to find for estimates (default is 5)]
             [MAXFN = maximum number of function evaluations (default is 1000)]
             [TRANSFORM = NONE or ABS (default is SIN transform)];
             /* Input to BROWNIE is exactly as described by Brownie et al.
             (1978:155-158) for programs ESTIMATE and BROWNIE, with the
             additional requirement that each card image must have a
             semicolon as the last non-blank character. */;
             /* Currently BROWNIE does not handle data of types 2 or 3 */;

PROC BMDPAR /* No modifiers */;

             INITIAL /* As in PROC ESTIMATE */;

             CONSTRAINTS /* As in PROC ESTIMATE */;

PROC IDENTIFIABLE
       [ADD = Constant to add for numerical derivative (Default is 0.05)]
       [MULTIPLY = Constant to multiply by for numerical derivative (Default is 1.05)];

             INITIAL /* As in PROC ESTIMATE */;

             CONSTRAINTS /* As in PROC ESTIMATE */;

PROC SIMULATE [NSIM = # of replications of each simulation (default is 5)]
                    [DETAIL (print details of each simulation,
                          with default of only simulation summaries)]
                    [SEED = random number seed (default is 7654321)];
                    [PARFILE = file name for simulated data output for later
                          analysis (default is no data output)]
                    [ERROR TEST (do not include simulations in data summaries
                          with warnings about convergence -- default to
                          include questionable convergence simulations)];

             INITIAL /* As in PROC ESTIMATE */;

             CONSTRAINTS /* As in PROC ESTIMATE */;

PROC SAMPLE SIZE /* Notation follows Brownie et al. 1978:190-193 */;
       S-BAR  = values of S /* Define average adult survival rates. */;
       S'-BAR = values of S' /* Define average young survival rates. */;
       F-BAR  = values of f /* Define average adult recovery rate. */;
       CV(S)  = values of CV of S /* Define coefficients of variation for values of S */;
       CV(S') = values of CV of S' /* Define coefficient of variation for values of S' */;
       K      = number of years /* Define number of years to conduct banding effort. */;

PROC STOP /* Stops execution. */;
```

Data Analysis

Three general tasks are required to estimate survival rates with the above procedure. First, the algebraic expressions must be read and the FORTRAN 77 subroutine constructed -- PROC MODEL performs this task. Second, the likelihood function must be numerically maximized by varying the parameter estimates for one or more sets of constraints on the parameters -- PROC ESTIMATE performs this task. Finally comparisons of parameter estimates by hypothesis tests must be made to identify the model appropriate for the observed data, performed by PROC TEST.

I will illustrate these procedures first with a simple example taken from Brownie et al. (1978), page 21. Ducks were banded for 3 years, and band recoveries summarized for 5 years. The input to run this model and the resulting output are shown in Fig. 1.

All input instructions read by Program SURVIV are echoed in the output with the identifying INPUT --- to delineate them. Thus on page 1 of the output in Fig. 1, PROC TITLE is called with a title for the run. Statements are separated by semicolons. Next PROC MODEL is called, with the number of parameters to be estimated set to 7. Additional comments are specified to clarify the input. PROC MODEL processes the observed data and the associated cell probability statements. Thus the next line of input is COHORT = 1603 with a comment to identify this cohort as the number of ducks banded in 1964. The COHORT card specifies the number of animals that are subject to mortality in the mortality categories that follow it. Therefore the next input statement specifies that 127 duck bands were returned, and the expected cell probability is S(3). That is, the observed multinomial cell value is 127, and the expected cell value is 1603*S(3), but the number of animals at risk of mortality is known from the COHORT statement, so only the expected cell probability is given. The colon (:) separates the observed number of recoveries and the expected cell probability.

The next statement continues to describe the fate of the 1603 ducks banded in 1964. Forty-four bands were recovered during the year 1965, with the expected cell probability being S(1)*S(4). The cell probability statements must be FORTRAN 77 readable, as these algebraic statements are used to construct the likelihood subroutine. The specification of observed recoveries and expected

cell probabilities continues for the 1964 cohort until 1968. At this time, 127 + 44 + 37 + 40 + 17 = 265 bands have been returned. Program SURVIV knows that the sum of the observed cells should add up to the number of animals specified on the proceeding cohort card. Because this is not the case, an additional cell is constructed with observed value equal to 1603 - 265 = 1338 ducks never seen again, and with expected cell probability equal to 1.0 minus the sum of the previous 5 cells. The sum of all the cell probabilities must be 1.0. Thus if a duck was never seen again (i.e., the band is not reported), then it falls into the last cell.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 01
                                                                                          Version 1.1(VMS) Aug., 1983
. . . . . .

INPUT --- PROC TITLE Banding Handbook Example from Page 21 of Brownie et al.(1978);

   CPU time in seconds for last procedure was     0.05


INPUT --- PROC MODEL NPAR=7 /* Banding Handbook Page 21 */ ;

INPUT ---     COHORT = 1603 /* BANDED 1964*/ ;
INPUT ---        127:S(3) /* BANDS RECOVERED IN 1964 */ ;
INPUT ---        44:S(1)*S(4) /* BANDS RECOVERED IN 1965 */ ;
INPUT ---        37:S(1)*S(2)*S(5) /* BANDS RECOVERED IN 1966 */ ;
INPUT ---        40:S(1)*S(2)*S(6) /* BANDS RECOVERED IN 1967 */ ;
INPUT ---        17:S(1)*S(2)*S(7) /* BANDS RECOVERED IN 1968 */ ;

INPUT ---     COHORT = 1595 /* BANDED 1965*/ ;
INPUT ---        62:S(4) /* Bands recovered in 1965 */ ;
INPUT ---        76:S(2)*S(5) /* Bands recovered in 1966 */ ;
INPUT ---        44:S(2)*S(6) /* Bands recovered in 1967 */ ;
INPUT ---        28:S(2)*S(7) /* Bands recovered in 1968 */ ;

INPUT ---     COHORT = 1157 /* BANDED 1966*/ ;
INPUT ---        82:S(5) /* BANDS RECOVERED IN 1966 */ ;
INPUT ---        61:S(6) /* BANDS RECOVERED IN 1967 */ ;
INPUT ---        24:S(7) /* BANDS RECOVERED IN 1968 */ ;

INPUT ---     LABELS;
INPUT ---        S(1)=Survival for 1964;
INPUT ---        S(2)=Survival for 1965;
INPUT ---        S(3)=RECOVERY FOR 1964;
INPUT ---        S(4)=RECOVERY FOR 1965;
INPUT ---        S(5)=RECOVERY FOR 1966;
INPUT ---        S(6)=Survival for 1966 and recovery 1967;
INPUT ---        S(7)=Survival for 1966-67 and recovery 1968;

   CPU time in seconds for last procedure was     1.48
```

Figure 1. Output from Program SURVIV for a banding analysis model from Brownie et al. (1978:21).

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 02
Banding Handbook Example from Page 21 of Brownie et al.(1978)                              Version 1.1(VMS) Aug., 1983
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

 INPUT --- PROC ESTIMATE   NSIG=5 MAXFN=750 NAME=SV&RC_SAME      /* COMBINATION OF SURVIVAL AND RECOVERY RATES
 INPUT --- CONSTANT BY TIME*/;

 INPUT ---    INITIAL;
 INPUT ---       ALL=0.05;
 INPUT ---    CONSTRAINTS;
 INPUT ---       S(1)=S(2);
 INPUT ---       S(3)=S(4);
 INPUT ---       S(3)=S(5);

     Number of parameters in model  =  7

     Number of parameters set equal =  3

     Number of parameters fixed     =  0

     Number of parameters estimated =  4

                                 Lower    Upper
      I   Parameter   S(I)       Bound    Bound  Label
     ---  ---------  ------     -----    -----  --------------------
      1       1      0.050      0.000    1.000  Survival for 1964
      2       1      0.050      0.000    1.000  Survival for 1965
      3       2      0.050      0.000    1.000  RECOVERY FOR 1964
      4       2      0.050      0.000    1.000  RECOVERY FOR 1965
      5       2      0.050      0.000    1.000  RECOVERY FOR 1966
      6       3      0.050      0.000    1.000  Survival for 1966 and recovery 1967
      7       4      0.050      0.000    1.000  Survival for 1966-67 and recovery 1968

    Final function value  2648.6431     (Error Return =   0)

    Number of significant digits       7

    Number of function evaluations   133

                                                                  95% Confidence Interval
      I   Parameter      S(I)          Standard Error        Lower              Upper
     ---  ---------  --------------  --------------  --------------  --------------
      1       1      0.64058338      0.34957855E-01  0.57206599      0.70910078
      2       1      0.64058338      0.34957855E-01  0.57206599      0.70910078
      3       2      0.60617526E-01  0.32176157E-02  0.54310999E-01  0.66924053E-01
      4       2      0.60617526E-01  0.32176157E-02  0.54310999E-01  0.66924053E-01
      5       2      0.60617526E-01  0.32176157E-02  0.54310999E-01  0.66924053E-01
      6       3      0.51111879E-01  0.47218499E-02  0.41857053E-01  0.60366704E-01
      7       4      0.24322205E-01  0.30891896E-02  0.18267393E-01  0.30377016E-01
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 03
Banding Handbook Example from Page 21 of Brownie et al.(1978)                             Version 1.1(VMS) Aug., 1983
```

Variance-Covariance matrix of estimates on diagonal and below,

Correlation matrix of estimates above diagonal.

	1	2	3	4	5	6	7
1	0.12220516E-02	1.0000000	-0.50834998	-0.50834998	-0.50834998	-0.47184568	-0.34320111
2	0.12220516E-02	0.12220516E-02	-0.50834998	-0.50834998	-0.50834998	-0.47184568	-0.34320111
3	-0.57179685E-04	-0.57179685E-04	0.10353051E-04	1.0000000	1.0000000	0.19792254	0.14396070
4	-0.57179685E-04	-0.57179685E-04	0.10353051E-04	0.10353051E-04	1.0000000	0.19792254	0.14396070
5	-0.57179685E-04	-0.57179685E-04	0.10353051E-04	0.10353051E-04	0.10353051E-04	0.19792254	0.14396070
6	-0.77885558E-04	-0.77885558E-04	0.30070566E-05	0.30070566E-05	0.30070566E-05	0.22295866E-04	0.13951651
7	-0.37062783E-04	-0.37062783E-04	0.14309442E-05	0.14309442E-05	0.14309442E-05	0.20350840E-05	0.95430924E-05

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	127	97.170	9.158	0 < P < 1
1	2	44	62.245	5.348	0 < P < 1
1	3	37	39.873	0.207	0 < P < 1
1	4	40	33.621	1.210	0 < P < 1
1	5	17	15.999	0.063	0 < P < 1
1	6	1338	1354.092	0.191	0 < P < 1
2	1	62	96.695	12.443	0 < P < 1
2	2	76	61.935	3.194	0 < P < 1
2	3	44	52.223	1.295	0 < P < 1
2	4	28	24.851	0.399	0 < P < 1
2	5	1385	1359.307	0.486	0 < P < 1
3	1	82	70.134	2.007	0 < P < 1
3	2	61	59.136	0.059	0 < P < 1
3	3	24	28.141	0.609	0 < P < 1
3	4	990	999.588	0.092	0 < P < 1

```
Total (Degrees of freedom =   8)      36.761
Pr(Larger Chi-square) = 0.0000
With pooling, Degrees of freedom =   8  Chi-square =     36.761
Pr(Larger Chi-square) = 0.0000

Log-likelihood = -52.874994

  CPU time in seconds for last procedure was    1.86
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 04
Banding Handbook Example from Page 21 of Brownie et al.(1978)                              Version 1.1(VMS) Aug., 1983
```

```
INPUT --- PROC ESTIMATE   NSIG=5 MAXFN=750 NAME=GENERAL /*General model*/;
INPUT ---     INITIAL;
INPUT ---     RETAIN=SV&RC_SAME ;
```

Number of parameters in model = 7

Number of parameters set equal = 0

Number of parameters fixed = 0

Number of parameters estimated = 7

I	Parameter	S(I)	Lower Bound	Upper Bound	Label
1	1	0.641	0.000	1.000	Survival for 1964
2	2	0.641	0.000	1.000	Survival for 1965
3	3	0.061	0.000	1.000	RECOVERY FOR 1964
4	4	0.061	0.000	1.000	RECOVERY FOR 1965
5	5	0.061	0.000	1.000	RECOVERY FOR 1966
6	6	0.051	0.000	1.000	Survival for 1966 and recovery 1967
7	7	0.024	0.000	1.000	Survival for 1966-67 and recovery 1968

Final function value 2632.5922 (Error Return = 0)

Number of significant digits 7

Number of function evaluations 190

I	Parameter	S(I)	Standard Error	95% Confidence Interval Lower	Upper
1	1	0.65386329	0.67817609E-01	0.52094078	0.78678580
2	2	0.63432469	0.65052567E-01	0.50682166	0.76182772
3	3	0.79226450E-01	0.67459754E-02	0.66004339E-01	0.92448562E-01
4	4	0.40103773E-01	0.41474639E-02	0.31974743E-01	0.48232802E-01
5	5	0.68816791E-01	0.60804365E-02	0.56899135E-01	0.80734446E-01
6	6	0.51171460E-01	0.50073002E-02	0.41357151E-01	0.60985768E-01
7	7	0.24350557E-01	0.31908973E-02	0.18096398E-01	0.30604715E-01

Variance-Covariance matrix of estimates on diagonal and below,

Correlation matrix of estimates above diagonal.

	1	2	3	4	5	6	7

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 05
Banding Handbook Example from Page 21 of Brownie et al.(1978)                            Version 1.1(VMS) Aug., 1983
. . . . . .

  |
1 | 0.45992280E-02-0.38874199    -0.70637676E-01-0.38549334     0.16916143E-13 0.72043515E-13 0.86797202E-13
  |
2 |-0.17150167E-02 0.42318365E-02-0.25947279E-13 0.11893140    -0.56544739    -0.51057168    -0.38126647
  |
3 |-0.32316449E-04-0.11386782E-16 0.45508185E-04 0.53900554E-13-0.13003798E-13 0.16998136E-13 0.21718938E-13
  |
4 |-0.10842813E-03 0.32088069E-04 0.15080669E-17 0.17201457E-04-0.36206355E-13-0.68325729E-13-0.84330358E-13
  |
5 | 0.69755521E-17-0.22366158E-03-0.53339598E-18-0.91306601E-18 0.36971708E-04 0.30982260     0.23135825
  |
6 | 0.24464762E-16-0.16631246E-03 0.57418214E-18-0.14189612E-17 0.94330357E-05 0.25073055E-04 0.20890532
  |
7 | 0.18782830E-16-0.79141792E-04 0.46751567E-18-0.11160391E-17 0.44888239E-05 0.33378434E-05 0.10181826E-04


 Cohort  Cell   Observed  Expected  Chi-square  Note
 ------  ----  --------  --------  ----------  -------------
    1      1       127   127.000       0.000  0 < P < 1
    1      2        44    42.034       0.092  0 < P < 1
    1      3        37    45.754       1.675  0 < P < 1
    1      4        40    34.022       1.050  0 < P < 1
    1      5        17    16.190       0.041  0 < P < 1
    1      6      1338  1338.000       0.000  0 < P < 1
    2      1        62    63.966       0.060  0 < P < 1
    2      2        76    69.625       0.584  0 < P < 1
    2      3        44    51.773       1.167  0 < P < 1
    2      4        28    24.637       0.459  0 < P < 1
    2      5      1385  1385.000       0.000  0 < P < 1
    3      1        82    79.621       0.071  0 < P < 1
    3      2        61    59.205       0.054  0 < P < 1
    3      3        24    28.174       0.618  0 < P < 1
    3      4       990   990.000       0.000  0 < P < 1
 ------------------------------------------------------------
 Total (Degrees of freedom =   5)       5.872
 Pr(Larger Chi-square) = 0.3189
 With pooling, Degrees of freedom =   5  Chi-square =      5.872
 Pr(Larger Chi-square) = 0.3189

 Log-likelihood = -36.824115

   CPU time in seconds for last procedure was    2.40
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 06
Banding Handbook Example from Page 21 of Brownie et al.(1978)                              Version 1.1(VMS) Aug., 1983
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

INPUT --- PROC ESTIMATE   NSIG=5 MAXFN=750 NAME=SURVL_SAME      /* 1964 SURVIVAL EQUALS 1965 SURVIVAL*/;

INPUT ---    INITIAL;

INPUT ---    RETAIN=GENERAL ;

INPUT ---    CONSTRAINTS;
INPUT ---       S(2)=S(1);

    Number of parameters in model  =  7

    Number of parameters set equal =  1

    Number of parameters fixed     =  0

    Number of parameters estimated =  6

                                 Lower    Upper
  I   Parameter   S(I)           Bound    Bound  Label
 ---  ---------  ------         -----    -----  --------------------
  1       1      0.654          0.000    1.000  Survival for 1964
  2       1      0.654          0.000    1.000  Survival for 1965
  3       2      0.079          0.000    1.000  RECOVERY FOR 1964
  4       3      0.040          0.000    1.000  RECOVERY FOR 1965
  5       4      0.069          0.000    1.000  RECOVERY FOR 1966
  6       5      0.051          0.000    1.000  Survival for 1966 and recovery 1967
  7       6      0.024          0.000    1.000  Survival for 1966-67 and recovery 1968

 Final function value  2632.6078     (Error Return =   0)

 Number of significant digits      10

 Number of function evaluations    168

                                                                    95% Confidence Interval
  I   Parameter      S(I)          Standard Error          Lower                 Upper
 ---  ---------  --------------  --------------  --------------  --------------
  1       1      0.64393595      0.36818149E-01  0.57177238      0.71609952
  2       1      0.64393595      0.36818149E-01  0.57177238      0.71609952
  3       2      0.79277320E-01  0.67417990E-02  0.66063394E-01  0.92491246E-01
  4       3      0.40325278E-01  0.39726728E-02  0.32538839E-01  0.48111717E-01
  5       4      0.68453790E-01  0.57011518E-02  0.57279533E-01  0.79628048E-01
  6       5      0.50901536E-01  0.47490351E-02  0.41593428E-01  0.60209645E-01
  7       6      0.24222110E-01  0.30925154E-02  0.18160780E-01  0.30283441E-01

 Variance-Covariance matrix of estimates on diagonal and below,
        Correlation matrix of estimates above diagonal.
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 07
Banding Handbook Example from Page 21 of Brownie et al.(1978)                            Version 1.1(VMS) Aug., 1983
```

	1	2	3	4	5	6	7
1	0.13555761E-02	1.0000000	-0.63570483E-01	-0.25020257	-0.54624638	-0.48761740	-0.35633115
2	0.13555761E-02	0.13555761E-02	-0.63570483E-01	-0.25020257	-0.54624638	-0.48761740	-0.35633115
3	-0.15779501E-04	-0.15779501E-04	0.45451854E-04	-0.13455097E-01	0.15415179E-01	0.13760657E-01	0.10055734E-01
4	-0.36596243E-04	-0.36596243E-04	-0.36036734E-06	0.15782129E-04	0.11355109	0.10136358	0.74072419E-01
5	-0.11466031E-03	-0.11466031E-03	0.59249810E-06	0.25717972E-05	0.32503132E-04	0.23272711	0.17006759
6	-0.85260233E-04	-0.85260233E-04	0.44057551E-06	0.19123620E-05	0.63010794E-05	0.22553334E-04	0.15181413
7	-0.40572111E-04	-0.40572111E-04	0.20965317E-06	0.91002055E-06	0.29984447E-05	0.22296127E-05	0.95636516E-05

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	127	127.082	0.000	0 < P < 1
1	2	44	41.625	0.136	0 < P < 1
1	3	37	45.501	1.588	0 < P < 1
1	4	40	33.834	1.124	0 < P < 1
1	5	17	16.100	0.050	0 < P < 1
1	6	1338	1338.859	0.001	0 < P < 1
2	1	62	64.319	0.084	0 < P < 1
2	2	76	70.307	0.461	0 < P < 1
2	3	44	52.280	1.311	0 < P < 1
2	4	28	24.878	0.392	0 < P < 1
2	5	1385	1383.216	0.002	0 < P < 1
3	1	82	79.201	0.099	0 < P < 1
3	2	61	58.893	0.075	0 < P < 1
3	3	24	28.025	0.578	0 < P < 1
3	4	990	990.881	0.001	0 < P < 1

```
Total (Degrees of freedom =   6)       5.901
Pr(Larger Chi-square) = 0.4343
With pooling, Degrees of freedom =   6  Chi-square =      5.901
Pr(Larger Chi-square) = 0.4343

Log-likelihood = -36.839708

  CPU time in seconds for last procedure was    2.91
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 08
Banding Handbook Example from Page 21 of Brownie et al.(1978)                            Version 1.1(VMS) Aug., 1983
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

 INPUT --- PROC ESTIMATE   NSIG=5 MAXFN=750 NAME=REC_SAME /*CONSTANT RECOVERY RATES*/;

 INPUT ---    INITIAL;

 INPUT ---    RETAIN=GENERAL ;

 INPUT ---    CONSTRAINTS;
 INPUT ---       S(3)=S(4);
 INPUT ---       S(3)=S(5);

     Number of parameters in model  =  7

     Number of parameters set equal =  2

     Number of parameters fixed     =  0

     Number of parameters estimated =  5

                                 Lower    Upper
      I   Parameter   S(I)       Bound    Bound   Label
     ---  ---------  ------     -----    -----   --------------------
      1       1      0.654      0.000    1.000   Survival for 1964
      2       2      0.634      0.000    1.000   Survival for 1965
      3       3      0.079      0.000    1.000   RECOVERY FOR 1964
      4       3      0.079      0.000    1.000   RECOVERY FOR 1965
      5       3      0.079      0.000    1.000   RECOVERY FOR 1966
      6       4      0.051      0.000    1.000   Survival for 1966 and recovery 1967
      7       5      0.024      0.000    1.000   Survival for 1966-67 and recovery 1968

    Final function value  2647.1385     (Error Return =   0)

    Number of significant digits       7

    Number of function evaluations   131

                                                                  95% Confidence Interval
      I   Parameter       S(I)          Standard Error          Lower          Upper
     ---  ---------  --------------  --------------  --------------  --------------
      1       1      0.56107126      0.53357772E-01  0.45649002      0.66565249
      2       2      0.72176072      0.63359611E-01  0.59757588      0.84594556
      3       3      0.60639881E-01  0.32256549E-02  0.54317597E-01  0.66962164E-01
      4       3      0.60639881E-01  0.32256549E-02  0.54317597E-01  0.66962164E-01
      5       3      0.60639881E-01  0.32256549E-02  0.54317597E-01  0.66962164E-01
      6       4      0.48934496E-01  0.47092640E-02  0.39704339E-01  0.58164654E-01
      7       5      0.23286071E-01  0.30247206E-02  0.17357618E-01  0.29214523E-01
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 09
Banding Handbook Example from Page 21 of Brownie et al.(1978)                            Version 1.1(VMS) Aug., 1983
```

Variance-Covariance matrix of estimates on diagonal and below,
Correlation matrix of estimates above diagonal.

	1	2	3	4	5	6	7
1	0.28470518E-02	-0.26501651	-0.29049126	-0.29049126	-0.29049126	-0.57322427E-01	-0.42469136E-01
2	-0.89594864E-03	0.40144403E-02	-0.32749735	-0.32749735	-0.32749735	-0.49397615	-0.36597788
3	-0.49997542E-04	-0.66932676E-04	0.10404849E-04	1.0000000	1.0000000	0.19732926	0.14619764
4	-0.49997542E-04	-0.66932676E-04	0.10404849E-04	0.10404849E-04	1.0000000	0.19732926	0.14619764
5	-0.49997542E-04	-0.66932676E-04	0.10404849E-04	0.10404849E-04	0.10404849E-04	0.19732926	0.14619764
6	-0.14403741E-04	-0.14739119E-03	0.29975223E-05	0.29975223E-05	0.29975223E-05	0.22177167E-04	0.18809952
7	-0.68541938E-05	-0.70137875E-04	0.14264072E-05	0.14264072E-05	0.14264072E-05	0.26793286E-05	0.91489349E-05

Cohort	Cell	Observed	Expected	Chi-square	Note
1	1	127	97.206	9.132	0 < P < 1
1	2	44	54.539	2.037	0 < P < 1
1	3	37	39.364	0.142	0 < P < 1
1	4	40	31.766	2.134	0 < P < 1
1	5	17	15.116	0.235	0 < P < 1
1	6	1338	1365.009	0.534	0 < P < 1
2	1	62	96.721	12.464	0 < P < 1
2	2	76	69.809	0.549	0 < P < 1
2	3	44	56.334	2.700	0 < P < 1
2	4	28	26.807	0.053	0 < P < 1
2	5	1385	1345.329	1.170	0 < P < 1
3	1	82	70.160	1.998	0 < P < 1
3	2	61	56.617	0.339	0 < P < 1
3	3	24	26.942	0.321	0 < P < 1
3	4	990	1003.280	0.176	0 < P < 1

```
Total (Degrees of freedom =   7)      33.985
Pr(Larger Chi-square) = 0.0000
With pooling, Degrees of freedom =   7  Chi-square =     33.985
Pr(Larger Chi-square) = 0.0000

Log-likelihood = -51.370480

  CPU time in seconds for last procedure was    1.44
```

Fig. 1 Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  12-JAN-84 19:43:42 Page 10
Banding Handbook Example from Page 21 of Brownie et al.(1978)                              Version 1.1(VMS) Aug., 1983
. . . . . .

 INPUT --- PROC TEST;

    Submodel     Name       Log-likelihood  NDF   G-O-F
    --------  ----------  --------------  ---  ------
        1     SV&RC_SAME   -52.874994       8  0.0000
        2     GENERAL      -36.824115       5  0.3189
        3     SURVL_SAME   -36.839708       6  0.4343
        4     REC_SAME     -51.370480       7  0.0000

    GENERAL    VS. SV&RC_SAME  Chi-square =    32.102   D.F. =  3  Pr(Larger Chi-square) = 0.0000

    SURVL_SAME VS. SV&RC_SAME  Chi-square =    32.071   D.F. =  2  Pr(Larger Chi-square) = 0.0000

    REC_SAME   VS. SV&RC_SAME  Chi-square =     3.009   D.F. =  1  Pr(Larger Chi-square) = 0.0828

    GENERAL    VS. SURVL_SAME  Chi-square =     0.031   D.F. =  1  Pr(Larger Chi-square) = 0.8598

    GENERAL    VS. REC_SAME    Chi-square =    29.093   D.F. =  2  Pr(Larger Chi-square) = 0.0000

    SURVL_SAME VS. REC_SAME    Chi-square =    29.062   D.F. =  1  Pr(Larger Chi-square) = 0.0000

* *  WARNING  * *   Sequence of models reinitialized to zero.

    CPU time in seconds for last procedure was    0.08

 INPUT --- PROC STOP /* End of this run. */ ;

    CPU time in minutes for this job was    0.17

        E X E C U T I O N   S U C C E S S F U L
```

Fig. 1 Continued.

PROC MODEL continues to process COHORT statements and their associated cell probability statements for the ducks banded in 1965 and 1966. Note that some of the parameters to be estimated occur in more than one cohort. This is reasonable because the survival rate of a duck banded in 1964 and one banded in 1965 should both be the same in 1966, assuming that the leg band is not changing the survival rate.

The LABELS statement is used to document the biological meaning of the parameters. Thus S(1) is shown to be the finite survival rate for the year 1964. S(3) is the recovery rate for 1964. These parameters correspond to S_1 and f_1 in Brownie et al. (1978:21). S(6) and S(7) are products of survival and recovery rates which are not identifiable. These "nuisance" parameters must be in the model to estimate S(1) through S(5), but are not of much value biologically.

When PROC MODEL reaches the end of its input (signified by the PROC ESTIMATE statement), it constructs the FORTRAN 77 subroutine and writes it to a disk file. Program SURVIV then exits, the FORTRAN 77 compiler is called to compile the subroutine, the loader is called to place the binary code into the core image, and Program SURVIV is started up again, only this time, the compile run option is not set on the execute line so that Program SURVIV assumes that the version of the likelihood subroutine in the core image corresponds to the input to PROC MODEL. Thus PROC MODEL does not stop execution when the PROC ESTIMATE statement is reached, but passes control to PROC ESTIMATE.

PROC ESTIMATE performs the numerical optimization of the likelihood function. Several parameters are specified on the statement. NSIG = 5 tells PROC ESTIMATE to estimate the parameters to 5 significant digits. MAXFN = 750 says that only 750 evaluations of the likelihood function are to be performed before an error is printed and optimization stopped. NAME=GENERAL gives this model a name (up to 10 characters) to identify it later in the PROC TEST output. All the parameters for PROC ESTIMATE have defaults, including NAME=SUBMODELii, where ii is the model number of this PROC ESTIMATE execution.

The INITIAL statement tells PROC ESTIMATE to initialize the parameter values in preparation for optimization. ALL = 0.05 sets all the values to 0.05, i.e., S(1) = 0.05, S(2) = 0.25, ..., S(7) = 0.05. S(1) = 0.5 and S(2) = 0.7 resets the values of S(1) and S(2).

Following the input to PROC ESTIMATE is the summary of the initial conditions for the upcoming optimization. The initial value of each parameter, the lower bound, the upper bound, and the label are summarized in a table. After the table, the results of the optimization procedure are

printed. No errors are reported, the number of significant digits in the estimates are 6, and 211 function cells were required. The next table summarizes the parameter values, standard errors and 95% confidence intervals. Then the variance-covariance and correlation matrix is printed for the parameter values. Finally, a table of the observed versus expected cell probabilities is printed, and the contribution of each cell to the overall chi-square goodness-of-fit statistic. If the model does not fit the data, this chi-square test will reject the null hypothesis. The NOTE column provides another method to check that the model was correctly optimized. The message $0 < P < 1$ indicates that the cell probability was in the interval [0 - 1]. Error messages are printed if the cell probability is not in the [0 - 1] interval.

The next statement is another run of PROC ESTIMATE, this time to estimate the model parameters with equal survival in 1964 and 1965, and equal recovery rates in 1964, 1965, and 1966. These equalities are set with the CONSTRAINTS statement. S(1) = S(2) sets survival rates for 1964 and 1965 equal. S(3) = S(4) and S(3) = S(5) sets 1964, 1965, and 1966 recovery rates equal.

These constraints are reflected in the summary of initial conditions, because only 4 parameters are to be estimated. The column labeled PARAMETER in the summary table on page 004 of the output (Fig. 1) indicates the relationship between S(1) and the parameter index. Thus S(1) and S(2) are both parameter 1, and S(3), S(4), and S(5) are all parameter 2.

In the summary of the estimation results, the values of S(1) and S(2) are identical, and likewise for S(3), S(4), and S(5). Similarly, the variance-covariance matrix and the correlation matrix reflects that some of the parameters are constrained to be equal.

Two additional runs of PROC ESTIMATE are made in the example output. In the first, the 1964 and 1965 survival rates are not constrained, but the 1964, 1965, and 1966 recovery rates are all constrained equal. Thus a series of 4 models has been generated. The most general model allows every identifiable survival and recovery rate to be estimated. The other three models force various constraints on the estimates.

PROC TEST (page 010 of the output in Fig. 1) helps decide which of the four models is appropriate for the observed data. Each model is summarized in a table giving the log-likelihood function value, the degrees of freedom of the model, and the chi-square goodness-of-fit significance probability. In the example, only the GENERAL and SURVL_SAME models fit the observed data. Both the models with recoveries constrained equal for 1964, 1965, and 1966 reject the goodness-of-fit null hypothesis.

The next 6 lines provide the likelihood ratio test results of all pairs of models that do not have equal degrees of freedom. Thus the first test suggests that the GENERAL model with 7 parameters does not fit the data much better than constraining survival rates by year to be equal, because the significance level of the chi-square statistic is not less than 0.05. However, tests of GENERAL versus either of the models with recovery rates constant by year strongly reject the null hypothesis, further suggesting that constant recovery rates do not fit the observed data.

Thus the biologists would conclude from this analysis that constant recovery rates are not valid for the observed data, but constant survival rates may be.

PROC ESTIMATE Fails

The chances that the numerical optimization procedure will not converge increase with the number of parameters, with parameter estimates against their boundaries, and with model complexity. Generally the failure of the procedure to converge will be obvious: the number of significant digits is less than what was requested, an error message is printed, and/or some parameters never changed from their initial value.

Generally when PROC ESTIMATE does not converge properly, a warning about the possible lack of parameter identifiability is printed. When this warning is received, the user should verify that each of the parameters can actually be estimated with the model and data input to SURVIV. I have not found a suitable numerical approach to determine parameter identifiability other than the error messages printed from PROC ESTIMATE. Occasionally, the numerical optimization procedure in

PROC ESTIMATE will converge, but the variance-covariance matrix of the parameter estimates is not positive-definite. Lack of positive-definiteness of the variance-covariance matrix is a strong indication that the problem lacks identifiability.

Determination of parameter identifiability with numerical methods is difficult because of the limited numerical precision of any calculations performed. That is, a large problem (many parameters to be estimated) will appear to lack identifiability, even though the parameters are actually identifiable. I have found no suitable method to distinguish numerical problems in a large or poorly conditioned problem from the case where the parameters really are not identifiable. Thus the user must carefully check the model input to SURVIV to verify that parameters are identifiable.

When PROC ESTIMATE does not produce reasonable answers, the user can try several things to correct the situation. The first is change the initial parameter estimates to values closer to the true values, i.e., make better initial guesses. Use the observed data to obtain these guesses rather than just setting the initial value to 0.5. Also, run PROC ESTIMATE with a constrained model to obtain better estimates, and use the INITIAL; RETAIN=_____ feature of PROC ESTIMATE to input the parameter estimates from this reduced model for the more complex model.

Second, PROC ESTIMATE allows an absolute value transformation that may improve convergence of the algorithm when one or more parameters are at their upper or lower boundaries. For example, if S(1) < 0.75 is specified as a constraint, and the optimization procedure wants to make S(1) > 0.75, a convergence problem may result. By specifying TRANSFORM = ABS on the PROC ESTIMATE statement, the difficulties with constrained parameters may disappear.

Finally, another procedure is available in SURVIV to generate input files for the BMDPAR program of the BMDP statistical package (Dixon 1981). Two files are generated for input to BMDPAR: BMDFUN (NOS), BMDFUN.FOR (VMS), or bmdfun.f (UNIX) contains the FORTRAN source code for the BMDPAR FUN subroutine; and BMDINP (NOS), BMDINP.DAT (VMS) or bmdinp.d (UNIX) contains the input to BMDPAR. PROC BMDPAR utilizes the same INITIAL and CONSTRAINT statements as PROC ESTIMATE and passes this information on to

the BMDPAR program. One advantage of using the BMDPAR program to perform the optimization is the greater flexibility to specify inequality constraints. Once the BMDPAR input file has been generated, the user can modify it to provide constraints not handled by SURVIV. Thus the user can modify the file of instructions to the BMDP-BMDPAR program to handle constraints such as survival < (1. - recovery). Verification of results from SURVIV with BMDPAR is also encouraged to guard against the possibility of a local maximum of the likelihood function being accepted as the global maximum.

Data Simulation and Sample Sizes

The preceding example illustrates the basic data analysis methods of Program SURVIV. Two additional procedures help design survival estimation studies.

PROC SIMULATE performs Monte Carlo simulations for the model defined in the preceding PROC MODEL statements. An example utilizing a simple biotelemetry experiment is shown in Fig. 2 and is also used in White (1983). The question to be answered in this simulation is whether 40 collars in year 1 and 50 collars in year 2 are enough effort to detect changes in survival rates of 0.1. Thus the first PROC ESTIMATE simulates 4 survival rates: 0.6, 0.7, 0.5, and 0.6. The second PROC ESTIMATE uses the same data, but constrains S(1) = S(2) and S(3) = S(4). Thus the PROC TEST procedure then tests for constant survival for years 1 and 2 and years 3 and 4.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:05:08 Page 01
                                                                                          Version 1.1(VMS) Aug., 1983
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

INPUT --- PROC TITLE Small Biotelemetry Example for Simulation in User's Manual;

   CPU time in seconds for last procedure was     0.04


INPUT --- PROC MODEL NPAR=4 /* Simple Biotelemetry Example */;

INPUT ---     COHORT = 40 /* Number of animals collared in year 1*/;
INPUT ---        0:(1.-S(1));
INPUT ---        0:S(1)*(1.-S(2));
INPUT ---        0:S(1)*S(2)*(1.-S(3));
INPUT ---        40:S(1)*S(2)*S(3);

INPUT ---     COHORT = 50 /* Number of animals collared in year 2*/;
INPUT ---        0:(1.-S(2));
INPUT ---        0:S(2)*(1.-S(3));
INPUT ---        0:S(2)*S(3)*(1.-S(4));
INPUT ---        50:S(2)*S(3)*S(4);

INPUT ---     LABELS;
INPUT ---        S(1)=Survival rate in year 1;
INPUT ---        S(2)=Survival rate in year 2;
INPUT ---        S(3)=Survival rate in year 3;
INPUT ---        S(4)=Survival rate in year 4;

   CPU time in seconds for last procedure was     1.04
```

Figure 2. Example of estimating survival rates from biotelemetry data when the data are simulated with PROC SIMULATE.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:05:08 Page 02
Small Bictelemetry Example for Simulation in User's Manual                                Version 1.1(VMS) Aug., 1983
. . . . . .

INPUT --- PROC SIMULATE NSIM=200 SEED=4567555 PARFILE=SIMDATA ERROR TEST ;

INPUT ---    INITIAL;
INPUT ---       S(1)=0.6;
INPUT ---       S(2)=0.7;
INPUT ---       S(3)=0.5;
INPUT ---       S(4)=0.6;

    Number of parameters in model  =  4

    Number of parameters set equal =  0

    Number of parameters fixed     =  0

    Number of parameters estimated =  4
     I   Parameter   S(I)    Bound    Bound  Label
    ---  ---------  ------   -----    -----  --------------------
     1       1      0.600    0.000    1.000  Survival rate in year 1
     2       2      0.700    0.000    1.000  Survival rate in year 2
     3       3      0.500    0.000    1.000  Survival rate in year 3
     4       4      0.600    0.000    1.000  Survival rate in year 4

INPUT --- PROC ESTIMATE NAME=GENERAL /* All parameters individually estimated */ ;
INPUT ---    INITIAL;
INPUT ---       S(1)=0.6;
INPUT ---       S(2)=0.7;
INPUT ---       S(3)=0.5;
INPUT ---       S(4)=0.6;

    Number of parameters in model  =  4

    Number of parameters set equal =  0

    Number of parameters fixed     =  0

    Number of parameters estimated =  4

                                    Lower    Upper
     I   Parameter   S(I)    Bound    Bound  Label
    ---  ---------  ------   -----    -----  --------------------
     1       1      0.600    0.000    1.000  Survival rate in year 1
     2       2      0.700    0.000    1.000  Survival rate in year 2
     3       3      0.500    0.000    1.000  Survival rate in year 3
     4       4      0.600    0.000    1.000  Survival rate in year 4
```

Fig. 2. Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:05:08 Page 03
Small Biotelemetry Example for Simulation in User's Manual                                Version 1.1(VMS) Aug., 1983
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -


 INPUT --- PROC ESTIMATE NAME=CONSTRAIN /* Sets of 2 parameters constrained. */ ;

 INPUT ---    INITIAL;
 INPUT ---       S(1)=0.6;
 INPUT ---       S(2)=0.7;
 INPUT ---       S(3)=0.5;
 INPUT ---       S(4)=0.6;

 INPUT ---    CONSTRAINTS;
 INPUT ---       S(1)=S(2);
 INPUT ---       S(3)=S(4);

     Number of parameters in model  =  4

     Number of parameters set equal =  2

     Number of parameters fixed     =  0

     Number of parameters estimated =  2

                                 Lower    Upper
      I   Parameter   S(I)       Bound    Bound  Label
     ---  ---------  ------     -----    -----  --------------------
      1       1      0.600      0.000    1.000  Survival rate in year 1
      2       1      0.600      0.000    1.000  Survival rate in year 2
      3       2      0.500      0.000    1.000  Survival rate in year 3
      4       2      0.500      0.000    1.000  Survival rate in year 4

    Parameter estimates are written to the file SIMDATA
    with the order being Replicate Number, Model Number,
    and the parameters (S(I),SE(S(I)),I=1,NPAR)
    The format used is '(8F10.6)', which generates (NPAR*2+2)/8+1 =  2 'CARDS' per model.

*** ERROR MESSAGE IER=130 FROM ROUTINE OPTMIZ

* *  WARNING  * *   Rounding errors became dominant before parameters estimated to NSIG digits for Model CONSTRAIN

* *  WARNING  * *   Check to be sure the parameters are identifiable, but the problem may just be ill-conditioned.

*** ERROR MESSAGE IER=130 FROM ROUTINE OPTMIZ

* *  WARNING  * *   Rounding errors became dominant before parameters estimated to NSIG digits for Model CONSTRAIN

* *  WARNING  * *   Check to be sure the parameters are identifiable, but the problem may just be ill-conditioned.
```

Fig. 2. Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:05:08 Page 04
Small Biotelemetry Example for Simulation in User's Manual                                Version 1.1(VMS) Aug., 1983
```

S I M U L A T I O N R E S U L T S

MODEL GENERAL NSIM = 200 Converged = 200

I	MEAN S(I)-Hat	SE S(I)-Hat	95% C. I. Lower	Upper	
1	0.60625000	0.54008596E-02	0.59566432	0.61683568	Survival rate in year 1
2	0.69703761	0.39232190E-02	0.68934810	0.70472712	Survival rate in year 2
3	0.50514662	0.47237913E-02	0.49588799	0.51440525	Survival rate in year 3
4	0.59308799	0.84027701E-02	0.57661856	0.60955741	Survival rate in year 4

I	MEAN SE(S(I)-Hat)	SE SE(S(I)-Hat)	95% C. I. Lower	Upper	
1	0.76255140E-01	0.19810598E-03	0.75866852E-01	0.76643427E-01	Survival rate in year 1
2	0.52897333E-01	0.20781961E-03	0.52490007E-01	0.53304660E-01	Survival rate in year 2
3	0.69079840E-01	0.22577465E-03	0.68637322E-01	0.69522358E-01	Survival rate in year 3
4	0.11440702	0.80088804E-03	0.11283728	0.11597676	Survival rate in year 4

Results of Goodness of Fit Tests

<0.01	<0.05	<0.10	<0.50
3	16	28	99

S I M U L A T I O N R E S U L T S

MODEL CONSTRAIN NSIM = 200 Converged = 197

I	MEAN S(I)-Hat	SE S(I)-Hat	95% C. I. Lower	Upper	
1	0.66448527	0.31448248E-02	0.65832141	0.67064912	Survival rate in year 1
2	0.66448527	0.31448248E-02	0.65832141	0.67064912	Survival rate in year 2
3	0.52493834	0.41833879E-02	0.51673890	0.53313778	Survival rate in year 3
4	0.52493834	0.41833879E-02	0.51673890	0.53313778	Survival rate in year 4

I	MEAN SE(S(I)-Hat)	SE SE(S(I)-Hat)	95% C. I. Lower	Upper	
1	0.43532547E-01	0.12374531E-03	0.43290007E-01	0.43775088E-01	Survival rate in year 1
2	0.43532547E-01	0.12374531E-03	0.43290007E-01	0.43775088E-01	Survival rate in year 2
3	0.60142105E-01	0.20428022E-03	0.59741716E-01	0.60542494E-01	Survival rate in year 3
4	0.60142105E-01	0.20428022E-03	0.59741716E-01	0.60542494E-01	Survival rate in year 4

Fig. 2. Continued.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:05:08 Page 05
Small Biotelemetry Example for Simulation in User's Manual                               Version 1.1(VMS) Aug., 1983
. . . . . .

Results of Goodness of Fit Tests
   <0.01  <0.05  <0.10  <0.50
 ---------------------------
      7     25     41    124

          Likelihood Ratio Test Results

                            <0.01  <0.05  <0.10  <0.50  <1.00
-------------------------------------------------------------
GENERAL     VS. CONSTRAIN       9     33     53    132    197

    CPU time in seconds for last procedure was  167.20

 INPUT --- PROC STOP /* Signal end of analysis */ ;

    CPU time in minutes for this job was    2.80

        E X E C U T I O N   S U C C E S S F U L
```

Fig. 2. Continued.

The DETAIL specification on PROC SIMULATE causes a detailed printout of each of the simulations. Thus parameter estimates and the chi-square goodness-of-fit table are both printed. If a large number of simulations are performed, the output produced will be very large. Thus DETAIL should only be used with NSIM = 10 or less.

The PARFILE = file name specification on PROC SIMULATE is used to name an output file to receive the estimates and associated standard errors for each of the parameters to be estimated for each of the PROC ESTIMATEs. This file might be used as input to a statistical package to perform a more through analysis of the simulations than the summary printed by PROC SIMULATE. The format of this file is documented in the output from PROC SIMULATE.

A random number seed to simulate data with PROC SIMULATE is provided in the SEED = value specification. Generally, the seed should be a 5 or 7 digit odd random integer. Speci-

fying the same seed for two PROC SIMULATEs will generate identical data if the same model is used.

PROC SAMPLE SIZE is used to estimate the number of animals to band based on the methods described in Brownie et al. (1978:190-193). The example shown in Fig. 3 duplicates the example in Brownie et al. (1978:186-193).

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:12:46 Page 01
                                                                                          Version 1.1(VMS) Aug., 1983
. . . . . .

INPUT --- PROC TITLE Sample Size Estimation for Banding Study;

   CPU time in seconds for last procedure was    0.04
INPUT --- PROC SAMPLE SIZE /* Sample size's for Brownie et al. (1978:192) example */;

INPUT ---    S-BAR=0.6;

INPUT ---    S'-BAR=0.5;

INPUT ---    F-BAR=0.07;

INPUT ---    CV(S)=0.04;

INPUT ---    CV(S')=0.04 0.07 0.03;

INPUT ---    K=2 10 1;

    SAMPLE SIZE ESTIMATION FOLLOWING BROWNIE ET AL. 1976:190-193

    NOTATION   INTERPRETATION
    --------   ------------------------------------------------------
     S-BAR     Mean adult survival rate per year
     S'-BAR    Mean young survival rate per year
     F-BAR     Mean adult recovery rate per year
     CV(S)     Coefficient of variation of mean adult survival rate
     CV(S')    Coefficient of variation of mean young survival rate
       K       Number of years to conduct banding effort
       M       Number of young to band each year
       N       Number of adults to band each year
```

Figure 3. Example of input to Program SURVIV for PROC SAMPLE SIZE and the output produced.

```
Program SURVIV - Survival Rate Estimation with User Specified Cell Probability Functions  11-JAN-84 19:12:46 Page 02
Sample Size Estimation for Banding Study                                                  Version 1.1(VMS) Aug., 1983
```

S-BAR	S'-BAR	F-BAR	CV(S)	CV(S')	K	N	M
0.60	0.50	0.07	0.04	0.04	2	22560	27269
0.60	0.50	0.07	0.04	0.04	3	5698	16597
0.60	0.50	0.07	0.04	0.04	4	2554	15982
0.60	0.50	0.07	0.04	0.04	5	1462	23514
0.60	0.50	0.07	0.04	0.04	6	959	736686
0.60	0.50	0.07	0.04	0.04	7	686	-16917
0.60	0.50	0.07	0.04	0.04	8	520	-7295
0.60	0.50	0.07	0.04	0.04	9	411	-4331
0.60	0.50	0.07	0.04	0.04	10	336	-2949
0.60	0.50	0.07	0.04	0.07	2	22560	6395
0.60	0.50	0.07	0.04	0.07	3	5698	2798
0.60	0.50	0.07	0.04	0.07	4	2554	1740
0.60	0.50	0.07	0.04	0.07	5	1462	1257
0.60	0.50	0.07	0.04	0.07	6	959	987
0.60	0.50	0.07	0.04	0.07	7	686	816
0.60	0.50	0.07	0.04	0.07	8	520	700
0.60	0.50	0.07	0.04	0.07	9	411	616
0.60	0.50	0.07	0.04	0.07	10	336	553

```
   CPU time in seconds for last procedure was    0.28
INPUT --- PROC STOP /* End of this run. */ ;

   CPU time in minutes for this job was    0.01

      E X E C U T I O N   S U C C E S S F U L
```

Fig. 3. Continued.

The first number in each of the specification cards [S-BAR, S'-BAR, F-BAR, CV(S), CV(S'), and K], provides the value for that parameter to be used in the sample size calculation. However, because a range of parameter values are usually required, two additional values can be used to specify a range of values. Thus S-BAR = 0.1 0.5 0.1 tells PROC SAMPLE SIZE to use a range of S from 0.1 to 0.5 in increments of 0.1. Note that specifying ranges for all 5 input parameters can result in many pages of sample sizes to be output.

Additional Procedures

PROC STOP is used to exit the program and is provided to stop execution in a data file when additional models are included in the file, but cannot be executed in this particular run because the wrong PROC MODEL has been loaded into core. PROC STOP allows the stacking of multiple models in an input file, but only running the first one. A text editor can be used to move models from within the input file to the top.

PROC BROWNIE will generate PROC ESTIMATE type output from input to the programs ESTIMATE and BROWNIE described in Brownie et al. (1978:155-158). To use SURVIV on this input, a semicolon must be put at the end of each card image, i.e., each card of input to the Brownie et al. programs is treated as a statement in SURVIV. PROC BROWNIE generates the appropriate COHORT and cell probability cards for input to PROC MODEL, lists these cards on the output, and then runs PROC MODEL to generate the estimation subroutine. Once the estimation subroutine is loaded, PROC BROWNIE calls PROC ESTIMATE to generate estimates and likelihood function values for the models appropriate to the type of input. Thus PROC BROWNIE can be viewed as a combination of PROC MODEL and PROC ESTIMATE statements. PROC BROWNIE will generate each of the models analyzed in the Brownie et al. programs, and if PROC TEST is used, test results between models can be generated. The big advantage of using SURVIV to analyze these models is that additional hypothesis tests can be performed by using PROC ESTIMATE to analyze models not specified in the Brownie et al. programs. For example, to test if survival is constant for years 1970-75 but different than years 1976-1980, the appropriate constraint cards can be used. The definitions of the S(I)'s must be read from a previous run of PROC BROWNIE unless the user is very familiar with the coding scheme used.

PROC IDENTIFIABLE is somewhat useful in locating which pair of parameters are most highly correlated. The input specifications ADD and MULTIPLY allow the user to determine how the parameter value is changed to calculate the numerical derivatives used in this process. Generally PROC IDENTIFIABLE is a last resort at determining the non-identifiable parameters in a model.

File Names and Execution Line

Program SURVIV utilizes five files: to read input from, to write output on, to construct the FORTRAN 77 subroutine on, to construct the BMDPAR FUN subroutine on, and to construct the BMDPAR input on. The default file names for VAX/VMS are SURVIN.DAT, SUPVLP.DAT, SUBROUT.FOR, BMDFUN.FOR, and BMDINP.DAT, for CDC/NOS they are SURVIN, SURVLP, SUBROUT, BMDFUN, and BMDINP, and for UNIX they are survin, survlp, subrout.f, bmdfun.f, and bmdinp.d, respectively. For DOS, the default input and output files are the keyboard and monitor, respectively. The FORTRAN 77 routine is constructed on the EST.FOR file. Other output files are the same as the VAX/VMS version of the program.

The input file can be modified on the execute line by specifying I=filename. Likewise, the output from Program SURVIV can be placed on file XYZ by specifying L=XYZ on the execution line. The subroutine output file and the BMDPAR files can be changed only by modifying the program. The DOS version of the program cannot read the execution line. Rather, SURVIV asks for the user to enter the execution line parameters from the keyboard after the code is executed.

Besides the I and L parameters on the execution line, three additional parameters can be specified. COMPILE RUN (for NOS just COMPILE) tells PROC MODEL to write the estimation subroutine to disk and stop execution, that is, the correct model has not yet been replaced in the core image. If COMPILE RUN is not specified, execution proceeds assuming that the correct model is in core. NOECHO causes the input lines to not be printed in the output. This option can save some paper when the output is printed, but is not advised because of the difficulty in locating errors in the input. LINES = # specifies the number of output lines to print per page, with the default LINES = 60.

Installation Guide for Mainframes

Program SURVIV is provided on a 9-track, ASCII, 1600 bpi, unlabeled tape with 3 files. The first file is the current source code for VAX/VMS, the second is the current source code for

CDC/NOS, and the third is the input for multiple examples that run correctly, including all of the examples shown in this manual. The three files are 80 character record lengths, blocked at 960 characters per block, giving 12 card images per block. To set up Program SURVIV on your system, dump the appropriate source code and the input data file from the tape. Because Program SURVIV is written in ANSI FORTRAN 77, few problems should be encountered in compiling the source code with an ANSI standard FORTRAN 77 compiler. Versions of the code are also available for the UNIX and LTSS operating systems upon request.

The first step to implement Program SURVIV is to create an object deck (binary) file of the entire program with the FORTRAN 77 compiler. This object file should be saved, because the likelihood function subroutine must be replaced every time a PROC MODEL constructs a new subroutine.

Next a procedure file should be written to execute the program twice for each run, first to generate the model subroutine, and then to execute the program with this subroutine replacing the default (null) model subroutine. The basic steps that this procedure should perform are:

- Execute SURVIV with option COMPILE RUN specified,
- Execute the FORTRAN compiler with the subroutine file generated in the previous step,
- Replace the new object deck of subroutine EST in the SURVIV object file, and
- Execute SURVIV again with the new EST subroutine.

Examples of this control language procedures for VAX/VMS and CDC/NOS are shown in Figs. 4 and 5, respectively. In both cases, 3 parameters are passed when the procedure is executed: input file name, output file name, and a shortcut flag to indicate that the current EST subroutine in the SURVIV object is correct for the PROC MODEL specifications in the input file. Thus if multiple runs are made with the same model, the overhead of writing a subroutine, compiling it, and replacing it in the SURVIV object are avoided by specifying the shortcut flag.

```
$ ! VAX/VMS Procedure file to execute SURVIV
$ ! with input from P1, output on P2, and P3
$ ! used to shortcut compilation and linking
$ ! of a new MODEL.
$ ON ERROR THEN EXIT
$ DATAFILE := "SURVIN.DAT"
$ IF P1 .NES. "" THEN DATAFILE := 'P1'
$ OUTFILE := "SUPVLP.LIS"
$ IF P2 .NES. "" THEN OUTFILE := 'P2'
$ ! Logical name SYS$DISK is defined as the user's path name
$ RUNSURV :== $SYS$DISK:SURVIV.EXE
$ IF P3 .NES. "" THEN GOTO SHORTCUT
$ ! Copy SURVIV object from system
$ COPY [SURVIV]SURVIV.OBJ SURVIV.OBJ
$ LINK SURVIV/NOMAP
$ RUNSURV I='DATAFILE' L='OUTFILE' COMPILE RUN
$ FORTRAN/NOLIST SUBROUT
$ LINK SUBROUT,SURVIV/EXECUTABLE
$ SHORTCUT: CONTINUE
$ RUNSURV I='DATAFILE' L='OUTFILE'
$ EXIT
```

Figure 4. Control language procedure for VAX/VMS operating system.

```
IFE,$SHORTCT$.NE.$YES$,SHORT.
ATTACH,SURVOBJ=SURVIV/UN=SURVIV.
REWIND(DATAFIL,SUBROBJ,OUTFILE)
RETURN(OUTFILE)
SURVOBJ(I=DATAFIL,L=OUTFILE,COMPILE)
FTN5(I=SUBROUT,L=0,B=SUBROBJ,REW)
LIBEDIT(I=0,L=0,B=SUBROBJ,P=SURVOBJ,N=SURVOB2)
ENDIF(SHORT)
RETURN(OUTFILE)
REWIND(DATAFIL)
SURVOB2(I=DATAFIL,L=OUTFILE)
REVERT. SURVIV SUCCESSFUL
EXIT.
REVERT,ABORT. *** SURVIV ABORTED ***
```

Figure 5. Cyber Control Language (CCL) procedure for CDC/NOS operating system.

Installation Guide for DOS Microcomputers

SURVIV is distributed on two 5 1/4 inch DSDD floppy diskettes. The first contains the source code with separate files for each subroutine. The second floppy contains the object code generated with the Ryan-McFarland FORTRAN 77 compiler. To run SURVIV, at least 512k of RAM is required, plus a hard disk. For most problems, the size of the SURVIV.EXE file exceeds 360k, thus the hard disk requirement. A batch file (SURVIVE.BAT) is included on the second floppy disk to execute SURVIV, including the compile run to create EST.FOR, executing the Ryan-McFarland compiler to generate EST.OBJ, recreating SURVIV.EXE, and running SURVIV again to perform the numerical estimation phase of the process. The batch file is interactive, telling the user what input to enter. Any DOS editor can be used to create the input file. Example input is included in the SURVIN file on the floppy diskettes. A copy of this user's manual is also included on the floppies as USERMAN.WP, to be printed with WordPerfect.

Setting Larger Program Dimensions

Program SURVIV has been set up with flexible array dimensions through the use of FORTRAN 77 PARAMETER statements. All the critical dimensions that would need to be changed for larger problems are in the INCLUDE file MODELC. These PARAMETERS are well documented with comment statements. Values which can be changed are MAXPAR (maximum number of parameters that can be estimated), MAXCHT (maximum number of COHORTS allowed in a model), MXCLAS (maximum number of probability cells within a cohort), MAXMOD (maximum number of models that can be generated with PROC ESTIMATE and then tested with PROC TEST), and MAXCHS (the maximum size of the character string holding the input buffer). DOS does not allow character strings larger than 255 characters, so MAXCHS is set to 255. This limitation means that statements longer than about 120 characters are not allowed. Also, cell probability expressions in PROC MODEL may not exceed 255 characters in the DOS version of SURVIV.

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